

IN THE CLAIMS

1. (previously presented) A recombinant chimer hepatitis B core (HBc) protein molecule up to about 515 amino acid residues in length that

(a) contains an HBc sequence of at least about 130 of the N-terminal 150 amino acid residues of the HBc molecule that include a peptide-bonded heterologous epitope or a heterologous linker residue for a conjugated epitope present in the HBc immunodominant loop,

(b) contains one to ten cysteine residues toward the C-terminus of the molecule from the C-terminal residue of the HBc sequence and within about 30 residues from the C-terminus of the chimer molecule [C-terminal cysteine residue(s)],

(c) contains a sequence of at least 5 amino acid residues from HBc position 135 through position 140 toward the HBc C-terminus,

said chimer molecules (i) containing no more than about 5 percent substituted amino acid residues in the HBc sequence as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149, (ii) self-assembling into particles that are substantially free of binding to nucleic acids on expression in a host cell, and said particles are more stable than are particles formed from otherwise identical HBc chimer molecules that lack said C-terminal cysteine residue(s) or in which a C-terminal cysteine residue present in the chimer molecules is replaced by another residue, wherein said particle stability is assayed as a measurement of the percentage of full length chimer molecules determined by Coomassie Blue stain of reducing buffer 15%SDS-PAGE results obtained after dilution of purified particles to a concentration of 1 mg/mL in aqueous 50 mM NaPO₄,

pH 6.8, with sodium azide added to a final concentration of 0.02% and incubation at 37° C for about 14 days.

2. (original) The recombinant HBc chimer protein molecule according to claim 1 wherein said peptide-bonded heterologous epitope or a heterologous linker residue for a conjugated epitope is a heterologous epitope.

3. (original) The recombinant HBc chimer protein molecule according to claim 2 wherein said heterologous epitope is a B cell epitope.

4. (original) The recombinant HBc chimer protein molecule according to claim 3 that contains a second heterologous epitope peptide-bonded to one of amino acid residues 1-4 of HBc.

5. (original) The recombinant HBc chimer protein molecule according to claim 3 wherein said B cell epitope is peptide-bonded at a position in the HBc sequence between amino acid residues 76 and 85, and at least 5 residues of the HBc sequence of positions 76 through 85 are present.

6. (original) The recombinant HBc chimer protein molecule according to claim 5 wherein the HBc sequence between amino acid residues 76 and 85 is present, but interrupted by said B cell epitope.

7. (original) The recombinant HBc chimer protein molecule according to claim 2 further including a peptide-bonded heterologous T cell epitope.

8. (original) The recombinant HBc chimer protein molecule according to claim 7 wherein said T cell epitope is peptide-bonded to the C-terminal HBc amino acid residue.

9. (original) The recombinant HBc chimer protein molecule according to claim 8 wherein said C-terminal cysteine residue(s) is present within five amino acid residues of the C-terminus of the HBc chimer protein molecule.

10-11. (cancelled)

12. (original) The recombinant HBc chimer protein molecule according to claim 1 wherein said chimer contains a heterologous linker residue for a conjugated epitope.

13. (original) The recombinant HBc chimer protein molecule according to claim 12 wherein said heterologous linker residue for a conjugated epitope is peptide-bonded at a position in the HBc sequence between amino acid residues 76 and 85, and at least 4 residues of the HBc sequence of positions 76 through 85 are present.

14. (original) The recombinant HBc chimer protein molecule according to claim 13 wherein the HBc sequence between amino acid residues 76 and 85 is present, but interrupted by said heterologous linker residue for a conjugated epitope.

15. (original) The recombinant HBc chimer protein molecule according to claim 14 that contains the HBc amino acid

residue sequence of position 1 through at least position 140, plus a single cysteine residue at the C-terminus.

16. (original) The recombinant HBc chimer protein molecule according to claim 15 wherein said chimer contains the HBc amino acid residue sequence of position 1 through position 149.

17. (original) The recombinant HBc chimer protein molecule according to claim 16 wherein said heterologous linker residue for a conjugated epitope is selected from the group consisting of a lysine, aspartic acid, glutamic acid, cysteine and a tyrosine residue.

18. (previously presented) A recombinant hepatitis B virus core (HBc) protein chimer molecule with a length of about 135 to about 515 amino acid residues that contains four peptide-linked amino acid residue sequence domains from the N-terminus that are denominated Domains I, II, III and IV, wherein

(a) Domain I comprises about 71 to about 100 amino acid residues whose sequence includes at least the sequence of the residues of position 5 through position 75 of HBc and optionally includes a heterologous epitope containing up to about 30 amino acid residues peptide-bonded to one of HBc residues 1-4;

(b) Domain II comprises about 5 to about 250 amino acid residues peptide-bonded to HBc residue 75 of Domain I in which (i) zero to all residues in a sequence of HBc positions 76 through 85 are present peptide-bonded to one to about 245 amino acid residues that are heterologous to HBc and constitute a heterologous epitope or a heterologous linker residue for a

conjugated epitope or (ii) one or more of residues 76 to 85 is absent;

(c) Domain III is an HBC sequence from position 86 through position 135 peptide-bonded to residue 85 of Domain II; and

d) Domain IV comprises (i) 5 through fourteen residues of a HBC amino acid residue sequence from position 136 through 149 peptide-bonded to the residue of position 135 of Domain III, (ii) one to ten cysteine residues [C-terminal cysteine residue(s)] within about 30 residues from the C-terminus of the chimera molecule, and (iii) zero to about 100 amino acid residues in a sequence heterologous to HBC from position 150 to the C-terminus, with the proviso that Domain IV contain at least 6 amino acid residues including said one to ten cysteine residues of (ii),

said chimera molecules self-assembling into particles on expression in a host cell, said particles being substantially free of binding to nucleic acids and more stable than are particles formed from an otherwise identical HBC chimera molecules that lack said C-terminal cysteine residue(s) or in which a C-terminal cysteine residue present in the chimera molecules is replaced by another residue, wherein said particle stability is assayed as a measurement of the percentage of full length chimera molecules determined by Coomassie Blue stain of reducing buffer 15%SDS-PAGE results obtained after dilution of purified particles to a concentration of 1 mg/mL in aqueous 50 mM NaPO_4 , pH 6.8, with sodium azide added to a final concentration of 0.02% and incubation at 37° C for about 14 days, and having an amino acid residue sequence in which no more than about 5 percent of the amino acid residues are substituted

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in the HBC sequence of the chimera as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149.

19. (original) The recombinant HBC chimera protein molecule according to claim 18 that contains two heterologous epitopes.

20. (original) The recombinant HBC chimera protein molecule according to claim 19 wherein said two heterologous epitopes are present in Domains I and II, II and IV or I and IV.

21. (original) The recombinant HBC chimera protein molecule according to claim 19 wherein one of said two heterologous epitopes is a B cell epitope.

22. (original) The recombinant HBC chimera protein molecule according to claim 19 wherein one of said two heterologous epitopes is a T cell epitope.

23. (original) The recombinant HBC chimera protein molecule according to claim 19 wherein one of said two heterologous epitopes is a B cell epitope and the other is a T cell epitope.

24. (original) The recombinant HBC chimera protein molecule according to claim 18 wherein said Domain I includes a heterologous epitope peptide-bonded to one of HBC residues 1-4.

25. (original) The recombinant HBC chimera protein molecule according to claim 24 wherein said heterologous epitope of Domain II is a B cell epitope.

26. (original) The recombinant HBc chimer protein molecule according to claim 25 wherein said sequence heterologous to HBc from position 150 to the C-terminus is a T cell epitope peptide-bonded to one of HBc residues 140-149.

27. (original) The recombinant HBc chimer protein molecule according to claim 18 wherein said heterologous linker residue for a conjugated epitope or a heterologous epitope is a heterologous epitope.

28. (original) The recombinant HBc chimer protein molecule according to claim 27 wherein said heterologous epitope comprises up to, about 245 amino acid residues.

29. (original) The recombinant HBc chimer protein molecule according to claim 28 wherein said heterologous epitope is a B cell epitope.

30. (original) The recombinant HBc chimer protein molecule according to claim 27 wherein said heterologous epitope contains 6 to about 50 amino acid residues.

31. (original) The recombinant HBc chimer protein molecule according to claim 27 wherein said heterologous epitope contains 20 to about 30 amino acid residues.

32. (original) The recombinant HBc chimer protein molecule according to claim 27 wherein said Domain IV comprises 1 to about 5 cysteine residues within about 30 residues from the C-terminus of the chimer molecule.

33. (original) The recombinant HBc chimer protein molecule according to claim 27 wherein the HBc sequence between amino acid residues 76 and 85 is present, but interrupted by said heterologous epitope.

34. (cancelled)

35. (original) The recombinant HBc chimer protein molecule according to claim 18 wherein said sequence heterologous to HBc from position 150 to the C-terminus is a T cell epitope peptide-bonded to one of HBc residues 140-149.

36. (original) The recombinant HBc chimer protein molecule according to claim 18 wherein said heterologous linker residue for a conjugated epitope or a heterologous epitope is a heterologous linker residue for a conjugated epitope.

37. (original) The recombinant HBc chimer protein molecule according to claim 36 wherein said heterologous linker residue for a conjugated epitope is selected from the group consisting of a lysine, aspartic acid, glutamic acid, cysteine and a tyrosine residue.

38. (original) The recombinant HBc chimer protein molecule according to claim 37 that contains a single cysteine residue at the C-terminus of the HBc chimer protein molecule.

39-41. (cancelled)

42. (previously presented) A recombinant hepatitis B virus core (HBc) protein chimer molecule with a length of about 175 to about 240 amino acid residues that contains four peptide-linked amino acid residue sequence domains from the N-terminus that are denominated Domains I, II, III and IV, wherein

(a) Domain I comprises about the sequence of the residues of position 1 through position 75 of HBc;

(b) Domain II comprises about 5 to about 55 amino acid residues peptide-bonded to HBc residue 75 of Domain I in which at least 4 residues in a sequence of HBc positions 76 through 85 are present peptide-bonded to 6 to about 50 amino acid residues that are heterologous to HBc and constitute a heterologous epitope;

(c) Domain III is an HBc sequence from position 86 through position 135 peptide-bonded to residue 85 of Domain II; and

d) Domain IV comprises (i) 5 through fourteen residues of a HBc amino acid residue sequence from position 136 through 149 peptide-bonded to the residue of position 135 of Domain III, (ii) a cysteine residue [C-terminal cysteine residue] within about 30 residues from the C-terminus of the chimer molecule, and (iii) zero to about 50 amino acid residues in a sequence heterologous to HBc from position 150 to the C-terminus,

said chimer molecules self-assembling into particles on expression in a host cell that exhibit a ratio of absorbance at 280 nm to 260 nm of about 1.2 to about 1.6 and are more stable than are particles formed from an otherwise identical HBc chimer molecules that lack said C-terminal cysteine residue or in which a C-terminal cysteine residue present in the chimer molecules is replaced by another residue, wherein said particle stability is assayed as a measurement of the percentage of full

length chimer molecules determined by Coomassie Blue stain of reducing buffer 15%SDS-PAGE results obtained after dilution of purified particles to a concentration of 1 mg/mL in aqueous 50 mM NaPO₄, pH 6.8, with sodium azide added to a final concentration of 0.02% and incubation at 37° C for about 14 days, and having an amino acid residue sequence in which no more than about 5 percent of the amino acid residues are substituted in the HBc sequence of the chimera as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149.

43. (original) The recombinant HBc chimera protein molecule according to claim 42 wherein said heterologous epitope of Domain II is a B cell epitope.

44. (original) The recombinant HBc chimera protein molecule according to claim 43 wherein said heterologous epitope contains 15 to about 50 amino acid residues.

45. (original) The recombinant HBc chimera protein molecule according to claim 43 wherein said heterologous epitope contains 20 to about 30 amino acid residues.

46. (original) The recombinant HBc chimera protein molecule according to claim 43 wherein the HBc sequence between amino acid residues 76 and 85 is present, but interrupted by said heterologous epitope.

47. (previously presented) The recombinant HBc chimera protein molecule according to claim 43 wherein said B cell epitope is an amino acid sequence present in a pathogen selected from the group consisting of *Streptococcus pneumonia*,

Cryptosporidium parvum, HIV, foot-and-mouth disease virus, influenza virus, *Yersinia pestis*, *Haemophilus influenzae*, *Moraxella catarrhalis*, *Porphyromonas gingivalis*, *Trypanosoma cruzi*, *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium berghi*, *Plasmodium yoelli*, *Streptococcus sobrinus*, *Shigella flexneri*, RSV, *Plasmodium Entamoeba histolytica*, *Schistosoma japonicum*, *Schistosoma mansoni*, and ebola virus.

48. (original) The recombinant HBc chimer protein molecule according to claim 43 wherein said sequence heterologous to HBc from position 150 to the C-terminus is a T cell epitope peptide-bonded to one of HBc residues 140-149.

49. (original) The recombinant HBc chimer protein molecule according to claim 48 wherein said T cell epitope is from the organism against which a contemplated chimer is to be used as an immunogen.

50. (original) The recombinant HBc chimer protein molecule according to claim 43 wherein said C-terminal cysteine residue is located within about five amino acid residues of the C-terminus of the chimer protein molecule.

51. (previously presented) Immunogenic particles comprising recombinant hepatitis B core (HBc) chimeric protein molecules, said chimeric protein molecules being up to about 515 amino acid residues in length, said chimeric protein molecules

(a) containing an HBc sequence of at least about 130 of the N-terminal 150 amino acid residues of the HBc molecule,

(b) (i) displaying one or more heterologous immunogenic epitopes at the N-terminus, HBc immunogenic loop or

C-terminus, or (ii) having a heterologous linker residue for a conjugated epitope in the HBc immunogenic loop,

(c) containing a sequence of at least 5 amino acid residues from HBc position 135 through position 140 toward the HBc C-terminus, and containing a cysteine residue at or near the C-terminus,

(d) containing no more than about 5 percent substituted amino acid residues in the HBc sequence as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149, said particle being substantially free of nucleic acid binding and exhibiting enhanced stability relative to particles comprised of otherwise identical proteins that are free of said cysteine residue, wherein said particle stability is assayed as a measurement of the percentage of full length chimera molecules determined by Coomassie Blue stain of reducing buffer 15%SDS-PAGE results obtained after dilution of purified particles to a concentration of 1 mg/mL in aqueous 50 mM NaPO₄, pH 6.8, with sodium azide added to a final concentration of 0.02% and incubation at 37° C for about 14 days.

52. (previously presented) The immunogenic particles according to claim 51 that exhibits a 280/260 absorbance ratio of about 1.2 to about 1.7.

53. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays an immunogenic epitope at the N-terminus.

54. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays an immunogenic epitope at the C-terminus.

55. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays an immunogenic epitope in the immunogenic loop.

56. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays a B cell immunogenic epitope.

57. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays a T cell immunogenic epitope.

58. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein displays separate B cell and T cell immunogenic epitopes.

59. (previously presented) The immunogenic particles according to claim 51 whose recombinant HBc chimeric protein has a heterologous linker residue for a conjugated epitope in the HBc immunogenic loop.

60. (previously presented) The immunogenic particles according to claim 59 wherein said heterologous linker residue for a conjugated epitope is selected from the group consisting of a lysine, aspartic acid, glutamic acid, cysteine and a tyrosine residue.

61. (previously presented) The immunogenic particles according to claim 60 wherein said heterologous linker residue for a conjugated epitope is conjugated to a hapten.

62. (previously presented) The immunogenic particles according to claim 61 wherein said hapten is an oligosaccharide.

63. (previously presented) Immunogenic particles comprising a plurality of recombinant chimeric hepatitis B core (HBc) protein molecules;

said recombinant chimeric HBc protein molecules having a length of up to about 515 amino acid residues that

(a) contain a HBc sequence of at least about 130 of the N-terminal 150 amino acid residues of the HBc molecule that include a peptide-bonded heterologous epitope or a heterologous linker residue for a conjugated epitope present in the HBc immunodominant loop, or a sequence of at least about 135 residues of the N-terminal 150 HBc amino acid residues,

(b) contain one to ten cysteine residues toward the C-terminus of the molecule from the C-terminal residue of the HBc sequence and within about 30 residues from the C-terminus of the chimera molecule [C-terminal cysteine residue(s)],

(c) contain a sequence of at least 5 amino acid residues from HBc position 135 through position 140 toward the HBc C-terminus,

said chimera molecules containing no more than 10 percent conservatively substituted amino acid residues in the HBc sequence, and

said particles being substantially free of binding to nucleic acids, and being more stable than are particles formed from an otherwise identical HBc chimera molecules that lack said

C-terminal cysteine residue(s) or in which a C-terminal cysteine residue present in the chimera molecules is replaced by another residue, wherein said particle stability is assayed as a measurement of the percentage of full length chimera molecules determined by Coomassie Blue stain of reducing buffer 15%SDS-PAGE results obtained after dilution of purified particles to a concentration of 1 mg/mL in aqueous 50 mM NaPO₄, pH 6.8, with sodium azide added to a final concentration of 0.02% and incubation at 37° C for about 14 days, and having an amino acid residue sequence in which no more than about 5 percent of the amino acid residues are substituted in the HBc sequence of the chimera as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149.

64. (previously presented) The immunogenic particles according to claim 63 that exhibit a ratio of absorbance at 280 nm to 260 nm of about 1.4 to about 1.6.

65. (previously presented) The immunogenic particles according to claim 63 wherein the length of said recombinant chimeric HBc protein molecules is about 175 to about 240 amino acid residues.

66. (previously presented) The immunogenic particles according to claim 63 wherein said peptide-bonded heterologous epitope or a heterologous linker residue for a conjugated epitope is a heterologous epitope.

67. (previously presented) The immunogenic particles according to claim 66 wherein said heterologous epitope is a B cell epitope.

68. (previously presented) The immunogenic particles according to claim 63 wherein the length of said recombinant chimeric HBc protein molecules is up to about 435 amino acid residues.

69. (previously presented) The immunogenic particles according to claim 63 that contains a second heterologous epitope peptide-bonded to one of amino acid residues 1-4 of HBc.

70. (previously presented) The immunogenic particles according to claim 67 wherein said B cell epitope is peptide-bonded at a position in the HBc sequence between amino acid residues 76 and 85, and at least 5 residues of the HBc sequence of positions 76 through 85 are present.

71. (previously presented) The immunogenic particles according to claim 70 wherein the HBc sequence between amino acid residues 76 and 85 is present, but interrupted by said B cell epitope.

72. (previously presented) The immunogenic particles according to claim 68 further including a peptide-bonded heterologous T cell epitope.

73. (previously presented) The immunogenic particles according to claim 72 wherein said T cell epitope is peptide-bonded to the C-terminal HBc amino acid residue.

74. (previously presented) The immunogenic particles according to claim 73 wherein said C-terminal cysteine

residue(s) is present within five amino acid residues of the C-terminus of the HBc chimer protein molecule.

75. (previously presented) The immunogenic particles according to claim 63 wherein said recombinant chimeric HBc protein molecules have a length of about 135 to about 515 amino acid residues and contains four peptide-linked amino acid residue sequence domains from the N-terminus that are denominated Domains I, II, III and IV, wherein

(a) Domain I comprises about 71 to about 100 amino acid residues whose sequence includes at least the sequence of the residues of position 5 through position 75 of HBc and optionally includes a heterologous epitope containing up to about 30 amino acid residues peptide-bonded to one of HBc residues 1-4;

(b) Domain II comprises about 5 to about 250 amino acid residues peptide-bonded to HBc residue 75 of Domain I in which (i) zero to all of the residues in a sequence of HBc positions 76 through 85 are present peptide-bonded to one to about 245 amino acid residues that are heterologous to HBc and constitute a heterologous epitope or a heterologous linker residue for a conjugated epitope or (ii) the sequence of HBc at positions 76 to 85 is present free from heterologous residues;

(c) Domain III is an HBc sequence from position 86 through position 135 peptide-bonded to residue 85 of Domain II; and

d) Domain IV comprises (i) 5 through fourteen residues of a HBc amino acid residue sequence from position 136 through 149 peptide-bonded to the residue of position 135 of Domain III, (ii) one to ten cysteine residues [C-terminal cysteine residue(s)] within about 30 residues from the C-terminus of the

chimer molecule, and (iii) zero to about 100 amino acid residues in a sequence heterologous to HBc from position 150 to the C-terminus, with the proviso that Domain IV contain at least 6 amino acid residues including said one to ten cysteine residues of (ii), said chimeric HBc protein having an amino acid residue sequence in which no more than about 5 percent of the amino acid residues are substituted in the HBc sequence as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149.

76. (previously presented) The immunogenic particles according to claim 75 that contains a heterologous linker residue for a conjugated epitope in Domain II and further includes a hapten linked to said heterologous linker residue.

77. (previously presented) The immunogenic particles according to claim 76 wherein said hapten is a B cell immunogen.

78. (previously presented) The immunogenic particles according to claim 63 wherein said recombinant chimeric HBc protein molecules have a length of about 175 to about 240 amino acid residues and contain four peptide-linked amino acid residue sequence domains from the N-terminus that are denominated Domains I, II, III and IV, wherein

(a) Domain I comprises about the sequence of the residues of position 1 through position 75 of HBc;

(b) Domain II comprises about 5 to about 55 amino acid residues peptide-bonded to HBc residue 75 of Domain I in which at least 4 residues in a sequence of HBc positions 76 through 85 are present peptide-bonded to 6 to about 50 amino acid residues that are heterologous to HBc and constitute a heterologous epitope;

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(c) Domain III is an HBc sequence from position 86 through position 135 peptide-bonded to residue 85 of Domain II; and

d) Domain IV comprises (i) 5 through fourteen residues of a HBc amino acid residue sequence from position 136 through 149 peptide-bonded to the residue of position 135 of Domain III, (ii) one to about five cysteine residues [C-terminal cysteine residue] within about 30 residues from the C-terminus of the chimera molecule, and (iii) zero to about 50 amino acid residues in a sequence heterologous to HBc from position 150 to the C-terminus,

said particles exhibiting a ratio of absorbance at 280 nm to 260 nm of about 1.4 to about 1.6, and said chimeric HBc protein having an amino acid residue sequence in which no more than about 5 percent of the amino acid residues are substituted in the HBc sequence as compared to a sequence of SEQ ID NO:246-251 from position 1 through 149.

79-115. (cancelled)